

RAW SEQUENCE LISTING

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Application Serial Number: 10|619,992
Source: IFW0
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/619,992

DATE: 06/22/2005

TIME: 09:19:38

Input Set : N:\Cr3\RULE60\10619992.raw

Output Set: N:\CRF4\06222005\J619992.raw

Gene and Uses

1 <110> APPLICANT: Hefeneider, Steven
 2 Merkins, Louise
 3 Bennett, Robert
 4 Seiss, Donald
 5 <120> TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding
 6 <130> FILE REFERENCE: 00-617-A
 7 <140> CURRENT APPLICATION NUMBER: US/10/619,992
 8 <141> CURRENT FILING DATE: 2003-07-15
 9 <150> PRIOR APPLICATION NUMBER: US/09/921,099
 10 <151> PRIOR FILING DATE: 2001-08-01
 11 <160> NUMBER OF SEQ ID NOS: 21
 12 <170> SOFTWARE: PatentIn version 3.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 4351
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (602)..(4174)
 21 <400> SEQUENCE: 1

22	agccaagtct tgtcagagat ttcctctttc aggtggcaaa gctgttttct tcacacttga	60
23	gtctctacaa tattgtttgg atcagtagtt tccaaagttc attaaactcct ggccatactt	120
24	tattatgttt tggggtagtg gttatccaag ggaaacactt ttttaaaciaa caaaacaaaa	180
25	aaaccgccca gcagtccaaa gtaattttgtg ttcctaaaaa tggaatatgg aaagttaatt	240
26	tgcttggttg atgtggctgt tgagaaaaat acataaaaagc tttgatgttt attatgtgag	300
27	caaccaatat aaatacagtt tagttgaaag gaacactatt aaggtattgt ttccaggcag	360
28	aatttcagaa atgtaattaa ttcagcaaat aggtttttta aaaaagacat ccaaaggtta	420
29	taaaattatt tagaagtatt ttaggtctga agctgtaata gttgacttaa gcaattaact	480
30	cttcaaagggt gaatgatgaa tatgtgggta attcatactt ttgtccattt cttagcttaca	540
31	aaacactaca cagcaaaaata atgatctgct agactgctaa cccgagcatc cagcttcac	600
32	a atg cct gtg cag gca gct caa tgg aca gaa ttt ctg tcc tgt cca atc	649
33	Met Pro Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile	
34	1 5 10 15	
35	tgc tat aat gaa ttt gat gag aat gtg cac aaa ccc atc agt tta ggt	697
36	Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly	
37	20 25 30	
38	tgt tca cac act gtt tgc aag acc tgc ttg aat aaa ctt cat cga aaa	745
39	Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys	
40	35 40 45	
41	gct tgt cct ttt gac cag act gcc atc aac aca gat att gat gta ctt	793
42	Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu	
43	50 55 60	
44	cct gtc aac ttc gca ctt ctc cag tta gtt gga gcc cag gta cca gat	841

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45	Pro	Val	Asn	Phe	Ala	Leu	Leu	Gln	Leu	Val	Gly	Ala	Gln	Val	Pro	Asp	
46	65					70					75					80	
47	cat	cag	tca	att	aag	tta	agt	aat	cta	ggt	gag	aat	aaa	cac	tat	gag	889
48	His	Gln	Ser	Ile	Lys	Leu	Ser	Asn	Leu	Gly	Glu	Asn	Lys	His	Tyr	Glu	
49					85					90					95		
50	gtt	gca	aag	aaa	tgc	gtt	gag	gat	ttg	gca	ctc	tac	tta	aaa	cca	cta	937
51	Val	Ala	Lys	Lys	Cys	Val	Glu	Asp	Leu	Ala	Leu	Tyr	Leu	Lys	Pro	Leu	
52					100				105					110			
53	agt	gga	ggt	aaa	ggt	gta	gct	agc	ttg	aac	cag	agt	gca	ctg	agc	cgt	985
54	Ser	Gly	Gly	Lys	Gly	Val	Ala	Ser	Leu	Asn	Gln	Ser	Ala	Leu	Ser	Arg	
55					115				120					125			
56	cca	atg	caa	agg	aaa	ctg	gtg	aca	ctt	gta	aac	tgt	caa	ctg	gtg	gag	1033
57	Pro	Met	Gln	Arg	Lys	Leu	Val	Thr	Leu	Val	Asn	Cys	Gln	Leu	Val	Glu	
58					130				135				140				
59	gaa	gaa	ggt	cgt	gta	aga	gcc	atg	cga	gca	gct	cgt	tcc	ctt	gga	gaa	1081
60	Glu	Glu	Gly	Arg	Val	Arg	Ala	Met	Arg	Ala	Ala	Arg	Ser	Leu	Gly	Glu	
61					145				150				155			160	
62	aga	act	gta	aca	gaa	ctg	ata	tta	cag	cac	cag	aac	cct	cag	cag	ttg	1129
63	Arg	Thr	Val	Thr	Glu	Leu	Ile	Leu	Gln	His	Gln	Asn	Pro	Gln	Gln	Leu	
64					165				170					175			
65	tct	gcc	aat	cta	tgg	gcc	gct	gtc	agg	gct	cga	gga	tgc	cag	ttt	tta	1177
66	Ser	Ala	Asn	Leu	Trp	Ala	Ala	Val	Arg	Ala	Arg	Gly	Cys	Gln	Phe	Leu	
67					180				185					190			
68	ggg	cca	gct	atg	caa	gaa	gag	gcc	ttg	aag	ctg	gtg	tta	ctg	gca	tta	1225
69	Gly	Pro	Ala	Met	Gln	Glu	Glu	Ala	Leu	Lys	Leu	Val	Leu	Leu	Ala	Leu	
70					195				200				205				
71	gaa	gat	ggt	tct	gcc	ctc	tca	agg	aaa	gtt	ctg	gta	ctt	ttt	gtt	gtg	1273
72	Glu	Asp	Gly	Ser	Ala	Leu	Ser	Arg	Lys	Val	Leu	Val	Leu	Phe	Val	Val	
73					210				215				220				
74	cag	aga	cta	gaa	cca	aga	ttt	cct	cag	gca	tca	aaa	aca	agt	att	ggt	1321
75	Gln	Arg	Leu	Glu	Pro	Arg	Phe	Pro	Gln	Ala	Ser	Lys	Thr	Ser	Ile	Gly	
76					225				230			235				240	
77	cat	gtt	gtg	caa	cta	ctg	tat	cga	gct	tct	tgt	ttt	aag	gtt	acc	aaa	1369
78	His	Val	Val	Gln	Leu	Leu	Tyr	Arg	Ala	Ser	Cys	Phe	Lys	Val	Thr	Lys	
79					245				250					255			
80	aga	gat	gaa	gac	tct	tcc	cta	atg	cag	ctg	aag	gag	gaa	ttt	cgg	agt	1417
81	Arg	Asp	Glu	Asp	Ser	Ser	Leu	Met	Gln	Leu	Lys	Glu	Glu	Phe	Arg	Ser	
82					260				265					270			
83	tat	gaa	gca	tta	cgc	aga	gaa	cat	gat	gcc	caa	att	gtt	cat	att	gcc	1465
84	Tyr	Glu	Ala	Leu	Arg	Arg	Glu	His	Asp	Ala	Gln	Ile	Val	His	Ile	Ala	
85					275				280				285				
86	atg	gaa	gca	gga	ctc	cgt	att	tca	cct	gaa	cag	tgg	tcc	tct	ctt	ttg	1513
87	Met	Glu	Ala	Gly	Leu	Arg	Ile	Ser	Pro	Glu	Gln	Trp	Ser	Ser	Leu	Leu	
88					290				295				300				
89	tat	ggt	gat	ttg	gct	cat	aaa	tca	cac	atg	cag	tct	atc	att	gat	aag	1561
90	Tyr	Gly	Asp	Leu	Ala	His	Lys	Ser	His	Met	Gln	Ser	Ile	Ile	Asp	Lys	
91					305				310				315			320	
92	cta	cag	tct	cca	gag	tca	ttt	gca	aag	agt	gtc	cag	gaa	ttg	aca	att	1609
93	Leu	Gln	Ser	Pro	Glu	Ser	Phe	Ala	Lys	Ser	Val	Gln	Glu	Leu	Thr	Ile	

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94		325		330		335		
95	ggt ttg caa cga aca ggt gac cca gct aac tta aat aga ctg agg cct							1657
96	Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro							
97		340		345		350		
98	cat tta gag ctt ctt gca aac ata gac cct aat cca gac gct gtt tca							1705
99	His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser							
100		355		360		365		
101	cca act tgg gag cag ctg gaa aat gca atg gta gct gtt aaa aca gta							1753
102	Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val							
103		370		375		380		
104	ggt cat ggc ctt gtg gac ttc ata caa aat tat agt aga aaa ggc cat							1801
105	Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His							
106		385		390		395		400
107	gag acc cct cag cct cag cca aac agc aaa tac aag act agc atg tgc							1849
108	Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys							
109		405		410		415		
110	cga gat ttg cga cag cag ggg ggt tgt cca cga gga aca aat tgt aca							1897
111	Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr							
112		420		425		430		
113	ttt gcc cat tct cag gaa gag ctt gaa aag tat cga tta agg aac aaa							1945
114	Phe Ala His Ser Gln Glu Glu Glu Lys Tyr Arg Leu Arg Asn Lys							
115		435		440		445		
116	aag atc aat gcc act gta aga acg ttt cct ctt cta aat aaa gtt ggt							1993
117	Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly							
118		450		455		460		
119	gta aac aac act gtc aca acc aca gcc gga aat gtc att tct gtc ata							2041
120	Val Asn Asn Thr Val Thr Thr Thr Ala Gly Asn Val Ile Ser Val Ile							
121		465		470		475		480
122	gga agt act gaa aca aca ggg aaa att gtt cca agt aca aac gga att							2089
123	Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile							
124		485		490		495		
125	tca aat gca gaa aac agt gtt tcc cag cta atc tca cgt agt act gac							2137
126	Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp							
127		500		505		510		
128	agt acc tta aga gct ctg gag acc gtg aag aaa gtg gga aag gtt ggc							2185
129	Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly							
130		515		520		525		
131	gct aat ggt cag aat gct gct ggg ccc tct gca gat tct gta act gaa							2233
132	Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu							
133		530		535		540		
134	aat aaa att ggt tct cca ccc aag act cct gta agt aat gta gca gct							2281
135	Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala							
136		545		550		555		560
137	acc tca gct ggg ccc tct aat gtt gga aca gag ctg aat tct gtg cct							2329
138	Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro							
139		565		570		575		
140	caa aaa tcc agc cca ttt cta act aga gta cca gta tat cct ccg cat							2377
141	Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His							
142		580		585		590		

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143	tct gaa aac att cag tat ttt caa gat cca agg act cag ata ccc ttt	2425
144	Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe	
145	595 600 605	
146	gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg	2473
147	Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr	
148	610 615 620	
149	gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat	2521
150	Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn	
151	625 630 635 640	
152	aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat	2569
153	Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp	
154	645 650 655	
155	cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac	2617
156	His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr	
157	660 665 670	
158	cag cct cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct	2665
159	Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser	
160	675 680 685	
161	gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct	2713
162	Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro	
163	690 695 700	
164	atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg	2761
165	Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met	
166	705 710 715 720	
167	gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat	2809
168	Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr	
169	725 730 735	
170	aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag	2857
171	Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu	
172	740 745 750	
173	cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag	2905
174	Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys	
175	755 760 765	
176	acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag	2953
177	Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln	
178	770 775 780	
179	tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca	3001
180	Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala	
181	785 790 795 800	
182	aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt	3049
183	Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg	
184	805 810 815	
185	gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat	3097
186	Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His	
187	820 825 830	
188	ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata	3145
189	Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile	
190	835 840 845	
191	aat gcc att gat tca gag ccc aaa gat gtc att gct aat tca aat gct	3193

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194	gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta	3241
195	Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu	
196	865 870 875 880	
197	ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt	3289
198	Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe	
199	885 890 895	
200	agt gat gga ccc atc atc tca aaa tgg ggt gcg att tcc aga tct tcc	3337
201	Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser	
202	900 905 910	
203	cgt aca ggt tac cat acc aca gat cct gtc cag gcc act gct tcc caa	3385
204	Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln	
205	915 920 925	
206	gga agt gcg act aag ccc atc agt gta tca gat tat gtc cct tat gtc	3433
207	Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val	
208	930 935 940	
209	aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca	3481
210	Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser	
211	945 950 955 960	
212	tca gca cac tat gtt gaa agg gac aga ttc att gtt act gat tta tct	3529
213	Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser	
214	965 970 975	
215	ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt	3577
216	Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu	
217	980 985 990	
218	cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct	3625
219	Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala	
220	995 1000 1005	
221	ttg gcc atg caa cag aag tgg aat tcc ctg gat gaa ggc cgt cac	3670
222	Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His	
223	1010 1015 1020	
224	ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gga	3715
225	Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly	
226	1025 1030 1035	
227	gag tta cag agt gat tat aca gaa gat gca aca gat act aaa cct	3760
228	Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro	
229	1040 1045 1050	
230	gat agg gat atc gag tta gag ctt tca gca ctt gat act gat gaa	3805
231	Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu	
232	1055 1060 1065	
233	cct gat gga caa agt gaa cca att gaa gag atc ttg gac ata cag	3850
234	Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln	
235	1070 1075 1080	
236	ctt ggt atc agt tct caa aat gat cag ttg cta aat gga atg gca	3895
237	Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala	
238	1085 1090 1095	
239	gtg gaa aat ggg cat cca gta cag cag cac caa aag gag cca cca	3940
240	Val Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro	

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6

VERIFICATION SUMMARY

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